

us-09-997-628-349.ra1

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OM protein - protein search, using sw model

Run on: June 7, 2004, 06:56:54 ; Search time 22 Seconds
(without alignments)
213.544 Million cell update

s/sec

Title: US-09-997-628-349
Perfect score: 496
Sequence: 1 MRGPGHPLLLGLLLVLGPSP.....KRCARLLTRLAVSPVCMEDK 9
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being pri
nted,
and is derived by analysis of the total score distribution.

SUMMARIES

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, Appli						

ALIGNMENTS

RESULT 1

US-09-029-755C-5

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; Sequence 5, Application US/09029755C
; Patent No. 6326477
; GENERAL INFORMATION:
; APPLICANT: ILMEN, Marja
; APPLICANT: SOEDERLUND, Hans
; APPLICANT: PENTTILA, Merja
; TITLE OF INVENTION: PROCESS FOR MODIFYING GLUCOSE REPRESSION
; FILE REFERENCE: Substitute Sequence Listing-09-029755
; Patent No. 6326477
; CURRENT APPLICATION NUMBER: US/09/029,755C
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: PCT/FI96/00463
; PRIOR FILING DATE: 1996-08-30
; PRIOR APPLICATION NUMBER: FI 954123
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Trichoderma reesei QM 9414
US-09-029-755C-5
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us-09-997-628-349.ra1

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; STREET: 460 Point San Bruno Blvd
;
; CITY: South San Francisco
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; STATE: California
;
; COUNTRY: USA
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; ZIP: 94080
;
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;
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: patin (Genentech)
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; APPLICATION NUMBER: US/08/442,248
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; FILING DATE: 15-MAY-1995
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; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/330128
;
; FILING DATE: 27-OCT-1994
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Torchia, Timothy E.
;
; REGISTRATION NUMBER: 36,700
;
; REFERENCE/DOCKET NUMBER: 920C4
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 415/225-8674
;
; TELEFAX: 415/952-9881

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OM protein - protein search, using sw model

Run on: June 7, 2004, 06:57:39 ; Search time 568 Seconds
(without alignments)
45.074 Million cell updates/sec

Title: US-09-997-628-349
Perfect score: 496
Sequence: 1 MRGPGHPLLLGLLLVLGPSP.....KRCARLLTRLAVSPVCMEDK 91

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 1155919

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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88	65.5	13.2	318	14	US-10-032-585-7357	Sequence 7357, Ap
89	65	13.1	336	14	US-10-128-714-8083	Sequence 8083, Ap
90	65	13.1	2412	16	US-10-408-765A-214	Sequence 214, App
91	64.5	13.0	389	14	US-10-138-098-33	Sequence 33, Appl
92	64.5	13.0	390	14	US-10-138-098-31	Sequence 31, Appl
93	64.5	13.0	842	14	US-10-138-098-40	Sequence 40, Appl
94	64.5	13.0	1006	14	US-10-138-098-45	Sequence 45, Appl
95	64.5	13.0	1064	14	US-10-138-098-43	Sequence 43, Appl
96	64	12.9	185	12	US-10-425-114-58759	Sequence 58759, A
97	64	12.9	408	14	US-10-205-032-34	Sequence 34, Appl
98	64	12.9	480	11	US-09-973-424A-55	Sequence 55, Appl
99	64	12.9	928	8	US-08-578-684-2	Sequence 2, Appli
100	64	12.9	953	14	US-10-412-277-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-989-722-349

; Sequence 349, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Db      61 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 91
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RESULT 2

US-09-989-723-349

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; Sequence 349, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
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OM protein - protein search, using sw model

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(without alignments)
437.671 Million cell updates/sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: pir2:*
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4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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64	58	11.7	1170	2	A72287	hypothetical prote
65	57.5	11.6	160	2	T33883	hypothetical prote
66	57.5	11.6	237	2	G72676	hypothetical prote
67	57.5	11.6	416	2	A88109	protein C46E10.9 [
68	57.5	11.6	481	2	A95278	hypothetical prote
69	57.5	11.6	1477	2	T18534	protein-tyrosine k
70	57.5	11.6	1722	1	I78879	retinoblastoma bin

71	57	11.5	99	2	T02626	hypothetical prote
72	57	11.5	168	2	H64034	hypothetical prote
73	57	11.5	244	2	S57042	hypothetical prote
74	57	11.5	292	2	E89846	hypothetical prote
75	57	11.5	412	2	T16480	hypothetical prote
76	57	11.5	528	2	T21682	hypothetical prote
77	57	11.5	605	2	JC5673	receptor tyrosine
78	57	11.5	610	2	I48612	developmental kina
79	57	11.5	626	2	I48614	developmental kina
80	57	11.5	975	2	I48974	receptor-protein t
81	57	11.5	998	2	JC5672	receptor tyrosine
82	57	11.5	998	2	I58351	receptor protein-t
83	57	11.5	1015	2	JC5263	transmembrane tyro
84	57	11.5	1015	2	JC5062	phogrin precursor
85	57	11.5	2171	2	E86342	hypothetical prote
86	57	11.5	3412	1	GNWVTB	genome polyprotein
87	56.5	11.4	119	2	T02375	finger protein BBF
88	56.5	11.4	140	2	T16574	hypothetical prote
89	56.5	11.4	143	2	G84471	En/Spm-like transp
90	56.5	11.4	209	2	H85062	hypothetical prote
91	56.5	11.4	232	2	AC3152	C factor [imported
92	56.5	11.4	232	2	H98135	probable Rossman f
93	56.5	11.4	407	2	T00989	hypothetical prote
94	56.5	11.4	632	2	H70339	NADH2 dehydrogenas
95	56.5	11.4	841	1	VGBE37	glycoprotein H - h
96	56.5	11.4	1388	2	T34157	hypothetical prote
97	56	11.3	177	2	S33166	protective antigen
98	56	11.3	209	2	A48388	glutathione S-tran
99	56	11.3	218	1	WZBEF4	gene 62 protein -
100	56	11.3	225	2	G89936	conserved hypothet

ALIGNMENTS

RESULT 1

B72658

hypothetical protein APE0690 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000

C;Accession: B72658

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba, S.; Ankai, A.; Kosugi, H.; Hosoyama, A.; Fukui, S.; Nagai, Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura, Y.; Nomura, N.; Sako, Y.; Kikuchi, H.

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix K1.

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: B72658

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-214 <KAW>

A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79666.1; PID:d1043452; PID:g5104351

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0690

C;Superfamily: Aeropyrum pernix hypothetical protein APE0690

Query Match 15.4%; Score 76.5; DB 2; Length 214;
Best Local Similarity 31.6%; Pred. No. 0.48;
Matches 24; Conservative 11; Mismatches 24; Indels 17; Gaps 3;

```
Qy      3 GPGHPLL-----LGLLLVLGPSPEQRVEIVPRDLRMKDKFL----KHLTGPLYFSP 49
      |||: ||      : | |||:|      |: || :: |      :|| || : ||
Db      47 GPGYNLLQHVVGYPPVVKYLALGPNP----PILLLDLLLRNHMLPKLLQRHLIGPPHESP 102

Qy      50 KCSKHFHRLYHNTRDC 65
      |: | | : |
Db      103 FSVLHYVALVHYSYDC 118
```

RESULT 2

T39863

zinc finger protein - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T39863

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, August 1997

A;Reference number: Z21886

A;Accession: T39863

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-565 <WOO>

A;Cross-references: EMBL:Z98270; PIDN:CAB10978.1; GSPDB:GN00067; SPDB:SPBC1D7.02

A;Experimental source: strain 972h-; cosmid c1D7

C;Genetics:

A;Gene: SPDB:SPBC1D7.02

A;Map position: 2

Query Match 14.2%; Score 70.5; DB 2; Length 565;
Best Local Similarity 40.0%; Pred. No. 6.3;
Matches 20; Conservative 3; Mismatches 14; Indels 13; Gaps 2;

```
Qy      46 YFSPKCSKHFHRLYHNTRD-----CTIPAYYKRCARL--LTRLA 82
      | | |:| |:| | | |      || | || :| ||| |
Db      26 YKCPLCTKAFYRLEHQTRHIRTHTGEKPHVCTFPGCAKRFSRDELTRHA 75
```

RESULT 3

A41694

regulatory protein creA - *Emericella nidulans*

C;Species: *Emericella nidulans*, *Aspergillus nidulans*

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Sep-1993

C;Accession: A41694

R;Dowzer, C.E.A.; Kelly, J.M.

Mol. Cell. Biol. 11, 5701-5709, 1991

A;Title: Analysis of the creA gene, a regulator of carbon catabolite repression
in *Aspergillus nidulans*.

A;Reference number: A41694; MUID:92017851; PMID:1922072

A;Accession: A41694

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <DOW>

Query Match 14.1%; Score 70; DB 2; Length 416;
Best Local Similarity 28.1%; Pred. No. 5.2;
Matches 25; Conservative 8; Mismatches 28; Indels 28; Gaps 3;

```
Qy      5 GHPLLLGLLLVLGPSPEQ RVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRD 64
      |  |  ::  | : | :  :  ||  |  |  :  |||  |  |
Db      38 GASLLPPMVKGARPAEEARQDLPRP-----YKCPLCERAFHRLEHQTRH 82

Qy      65 -----CTIPAYYKRCARL--LTR 80
      |  |  ||  :  |  ||
Db      83 IRTHTGEKPHACQFPGCSKRFSRDELTR 111
```

RESULT 4

T27523

hypothetical protein ZC373.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T27523

R;Kershaw, J.

submitted to the EMBL Data Library, April 1995

A;Reference number: Z20382

A;Accession: T27523

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-284 <WIL>

A;Cross-references: EMBL:Z49131; PIDN:CAA88977.1; GSPDB:GN00028; CESP:ZC373.5

A;Experimental source: clone ZC373

C;Genetics:

A;Gene: CESP:ZC373.5

A;Map position: X

A;Introns: 26/3; 75/2; 114/1; 236/2

Query Match 13.9%; Score 69; DB 2; Length 284;
Best Local Similarity 31.6%; Pred. No. 4.5;
Matches 31; Conservative 13; Mismatches 36; Indels 18; Gaps 6;

```
Qy      1 MRGPGHPL--LLGLLLVLGPSPEQ RVEIVPRDL---RMKDKF-----LKHLTGPLYFSP 49
      |||  |  :  :  |  ::  ||  | :  |  ::  |||  |  :
Db      46 MRGSGGAMGCISGSELMISPSALQKERIREQDV FVYNMKDKTEVQRPPNKRIT-----VS 100

Qy      50 KCSKHFHRLYHNT-RDCTIPAYYKRCARLLTRLAVSPV 86
      ||  |  :  |  :  |  :  ||  | :  :  |  |
Db      101 SCSVLFSLLMKETGSECVIHTHSK-CANLITQLIKSNV 137
```

RESULT 5

B84104

transcription regulator (AraC/XylS family) BH3634 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: B84104

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirama, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: B84104
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-300 <STO>
 A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07353.1; GSPDB:GN00137
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH3634

Query Match 13.9%; Score 69; DB 2; Length 300;
 Best Local Similarity 34.9%; Pred. No. 4.7;
 Matches 22; Conservative 4; Mismatches 17; Indels 20; Gaps 3;

```
Qy      32 RMKDKFLKHLTGPL-----YFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLT 79
      | |  || |:          ||      |||||: | ||: | || | ||
Db      9 RAIDYIETHLHEPISLEKVAAHASYSYF-----HFHRLFKATVGCTMSEYIKR--RRLT 60

Qy      80 RLA 82
      : |
Db      61 KAA 63
```

RESULT 6

JN0785
 Carbon catabolite repressor protein - *Aspergillus niger*
 C;Species: *Aspergillus niger*
 C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000
 C;Accession: JN0785
 R;Drysdale, M.R.; Kolze, S.E.; Kelly, J.M.
 Gene 130, 241-245, 1993
 A;Title: The *Aspergillus niger* carbon catabolite repressor encoding gene, *creA*.
 A;Reference number: JN0785; MUID:93366180; PMID:8359691
 A;Accession: JN0785
 A;Molecule type: DNA
 A;Residues: 1-427 <DRY>
 A;Cross-references: GB:L03811; NID:g166497; PIDN:AAA32690.1; PID:g166498
 C;Comment: This protein plays a role as a negatively acting repressor protein regulating carbon catabolite repression.
 C;Genetics:
 A;Gene: *CreA*
 C;Keywords: DNA binding; repressor; transcription regulation; zinc finger
 F;73-128/Region: zinc finger

Query Match 13.9%; Score 69; DB 2; Length 427;
 Best Local Similarity 28.7%; Pred. No. 6.8;
 Matches 25; Conservative 7; Mismatches 23; Indels 32; Gaps 4;

```
Qy      7 PLLLLLLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRD-- 64
      ||: |  |: |: : :||          | | | : |||| | ||
Db     56 PLMKG----ARPATEEVQRDLPRP-----YKCPLCDRAFHRLEHQTRHIR 96
```